REMARKS

Favorable reconsideration of the subject application is respectfully requested in view of the above amendments and the following remarks. Following the amendments, claims 2, 5, 6, 8-16 and 31-35 are under consideration, with claims 2, 5, 6, 8, 13 and 31-35 being in independent format.

As requested by the Examiner, the title of the application has been amended to more closely represent the presently claimed subject matter. In addition, the specification has been amended to remove hyperlinks. Claim 2 has been amended to recite oligonucleotide probes and primers comprising at least 20 contiguous residues complementary to 20 contiguous residues of SEQ ID NO: 2076. Support for this amendment may be found on page 32, lines 22-25, of the specification as originally filed. Claim 33 has been amended to correct a minor typographical error. Specifically, reference to SEQ ID NO: 1076 has been replaced with reference to SEQ ID NO: 2076. Claim 35, drawn to polynucleotides encoding an amino acid sequence comprising SEQ ID NO: 2249, has been added. Support for newly added claim 35 may be found on page 36, lines 1-9, and throughout the specification as originally filed.

It is urged that support for all the above amendments may be found throughout the specification as originally filed and that none of the amendments constitute new matter.

Claim Objection

The Examiner has objected to claim 33 as reciting SEQ ID NO: 1076 instead of SEQ ID NO: 2076. As noted above, this typographical error has been corrected.

Information Disclosure Statement

The Examiner states that several of the references included in the PTO-1449 form filed on August 16, 2000, were not considered "because the international search report and GenBank data base are not required to be listed on PTO-1449". While, applicants agree with the Examiner's position regarding the International Search Report, they strongly disagree with the Examiner's position on the Genbank database accessions.

Applicants have a duty to disclose to the Patent Office prior art references and information that may be relevant to the patentability of an invention. 37 CFR §1.98 clearly states that an information disclosure statement shall include "a list of all patents, publications, applications, **or other information** submitted for consideration by the Office" (emphasis added). As stated in §609 of the Manual of Patent Examining Procedure (MPEP), "the examiner has an obligation to consider

the information" submitted in an information disclosure statement satisfying the requirements of 37 CFR §1.97 and 37 CFR §1.98. Applicants thus respectfully request that the Examiner make the Genbank accessions disclosed in the information disclosure statement filed on August 16, 2000, of record in the present application.

Claim Rejections under 35 USC §112, first paragraph.

The Examiner has rejected claims 2, 5, 6, 8-16 and 31-34 as lacking an enabling disclosure. Specifically, the Examiner has asserted that the disclosure is enabling only for claims limited to isolated polynucleotides consisting of SEQ ID NO: 2076. This rejection is respectfully traversed.

In response to the Restriction Requirement, applicants elected claims to the polynucleotide of SEQ ID NO: 2076. The isolation of SEQ ID NO: 2076 from *Eucalyptus grandis* is described in Example 1 of the specification (page 34, line 27 - page 36, line 9). As clearly stated in the specification on page 36, lines 2-9, the amino acid sequence encoded by SEQ ID NO: 2076 is provided in SEQ ID NO: 2249. As noted in Table 1 (page 14) of the specification, SEQ ID NO: 2076 encodes a transcription factor of the Myb family. As noted in Table 2 (page 24, line 6 - page 25, line 1, of the specification), two DNA-binding domains contained within the amino acid sequence of SEQ ID NO: 2249 are provided in SEQ ID NO: 2346 and 2347.

Applicant notes that, as stated in §2164.01(a) of the MPEP, the level of predictability in the art is only one of many factors to be considered when determining whether or not a disclosure satisfies the enablement requirement and that other factors to be considered include, but are not limited to, "the level of one of ordinary skill in the art" and "the amount of direction provided by the inventor". It is noted that the level of skill in the field of biotechnology is generally accepted to be quite high. §2164.01 of the MPEP also states "[t]he fact that experimentation may be complex does not necessarily make it undue if the art typically engages in such experimentation".

The instant specification clearly teaches methods for determining the percentage of identity of two sequences (*see* page 18, line 13 - page 20, line 12), together with the preparation of DNA constructs comprising the inventive polynucleotides (*see* page 23, line 25 to page 29, line 4) and methods for using such DNA constructs to modify gene expression in plants (*see* page 29, line 5 - page 31, line 19, and Example 3, page 37, lines 1-29). Furthermore, as evidenced by Martin and Paz-Ares (Trends Genet., 1997, *13*:67-73) and Reichmann et al. (Science, 2000, *290*:2105-2110; copes enclosed for the Examiner's convenience), it is well known in the art that MYB transcription factors contain DNA-binding domains showing a high level of conservation. As noted above, the

sequences of the DNA binding domains contained within the polypeptide encoded by SEQ ID NO: 2076 are provided in SEQ ID NO: 2346 and 2347. Given this information and the level of knowledge within the art, one of skill in the art would clearly be able to determine the location of the regions within SEQ ID NO: 2076 that correspond to these DNA binding domains.

It is thus urged that, on being provided with the instant specification, one of skill in the art to which the present invention pertains would clearly be able to prepare both polynucleotides comprising SEQ ID NO: 2076 and the polynucleotides recited in claims 33-35 and 5, determine whether the polypeptides encoded by such polynucleotides include the DNA binding domains characteristic of Myb transcription factors and therefore possess MYB transcription factor activity, and employ such polynucleotides in the inventive DNA constructs to modify gene expression in a plant. It is also urged that such studies, while being potentially time-consuming and tedious, do not constitute undue experimentation, and further that such studies are routinely carried out by those of skill in the art of plant and molecular biology.

Applicants respectfully submit that all the presently pending claims fully satisfy the enablement requirements of 35 USC §112, first paragraph, and that the rejection of the claims under 35 USC §112, first paragraph, may be properly withdrawn.

Claim Rejections under 35 USC §112, second paragraph.

Claim 33 stands rejected under 35 USC §112, second paragraph, as being indefinite. Specifically, the Examiner has objected to the term "degeneratively equivalent to SEQ ID NO: 2076". This rejection is respectfully traversed.

Applicants submit that one of skill in the art to which the present invention pertains would clearly understand that the phrase "degeneratively equivalent" encompasses polynucleotides that differ from a specific polynucleotide but that, due to the degeneracy of the genetic code, encode the same amino acid sequence. This is particularly true in view of the teaching at page 21, lines 15-17 of the instant specification.

It is thus urged that one of skill in the art would be able to clearly determine the metes and bounds of the presently pending claims and that this rejection of claim 33 under 35 USC §112, second paragraph, may be properly withdrawn.

Claim Rejections under 35 USC §102

Claims 2 and 31-34 stand rejected under 35 USC §102(b) as being fully taught by Uimari et al (The Plant Journal, 1997, 12(6):1273-1284). Specifically, the Examiner asserts that the DNA sequence of Uimari et al. "comprises SEQ ID NO: 2076". This rejection is respectfully traversed.

SEQ ID NO: 2076 is 862 nucleotides long. The comparison between SEQ ID NO: 2076 and the sequence of Uimari et al. provided with the Office Action starts at nucleotide 64 of SEQ ID NO: 2076 and ends at nucleotide 404, and thus only represents a comparison of the sequence of Uimari et al. with **part** of SEQ ID NO: 2076. This is clearly apparent from the comparison of the full-length sequence of SEQ ID NO: 2076 with the full-length sequence of Uimari et al. submitted with the Declaration of Dr. Elizabeth Visser filed herewith. Furthermore, in the region of overlap between SEQ ID NO: 2076 and the sequence of Uimari et al., there are several residues in the Uimari et al. sequence that do not match the corresponding nucleotide of SEQ ID NO: 2076. Applicants note that, for a reference to be prior art under 35 USC §102, every feature of the claimed invention must be disclosed in the reference (*see*, MPEP 706.02 and Atlas Powder v. E.I. du Pont, 750 F.2d 1569, 224 USPQ 409 (Fed. Cir. 1984)). The exact sequence of SEQ ID NO: 2076 is clearly **not** contained with the Uimari et al. sequence, and thus Uimari et al. do not teach every feature of pending claims 31 and 32.

With regard to claim 33, the nucleic acid search report simply shows that SEQ ID NO: 2076 and the Uimari et al. sequence show 80.9% local similarity over a specific portion of SEQ ID NO: 2076. As evidenced by the Declaration of Dr. Elizabeth Visser, submitted herewith, the percentage identity of SEQ ID NO: 2076 to the sequence of Uimari et al., determined as described in the specification (see, for example, page 18, lines 19-29), is less than 35%. Thus the sequence of Uimari et al. does not teach or suggest sequences having at least 75%, 90% or 95% identity to SEQ ID NO: 2076 as recited in pending claim 33.

With regard to claim 34, the term "x-mer" is defined on page 22, lines 16-31, of the specification as "a sequence comprising at least a specified number ("*x*") of contiguous residues" of the inventive sequence. The Uimari et al. sequence does not include regions of at least 200, 100, 40 or 20 contiguous residues that are identical to regions of at least 200, 100, 40 or 20 contiguous residues of SEQ ID NO: 2076. The cited reference therefore does not teach or suggest sequences and is not prior art under 35 USC §102 to claim 34. Similarly, Uimari et al. do not teach or suggest oligonucleotide probes or primers that contain at least 20 contiguous residues complementary to 20 contiguous residues of SEQ ID NO: 2076 as recited in amended claim 2.

It is thus urged that Uimari et al. do not teach or suggest the presently claimed invention, and that the rejection of claims 2 and 31-34 under 35 USC §102(b) may be properly withdrawn.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "Version with Markings to Show Changes Made."

Early consideration and allowance of the pending claims is respectfully requested.

Respectfully submitted,

Janet Sleath

Janet Sleath
Registration No. 37,007

February 7, 2003
SPECKMAN LAW GROUP

Version with Markings to Show Changes Made

In the specification:

On page 1, line 3, the present title has been replaced with the following new title:
--POLYNUCLEOTIDES FOR USE IN THE MODIFICATION OF GENE TRANSCRIPTION--

The paragraph beginning on page 17, line 14, has been replaced with the following amended paragraph:

--The polynucleotides identified as SEQ ID NOS: 1-591, 1183-1912 and 1931-2106 may contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are available, for example, on the Internet [at http://www.ncbi.nlm.nih.gov/gorf/gorf.html]. [Additionally,] Additional tools and software for ORF analysis[, for example, including] include GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN[, are suitable]. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.--

The paragraph beginning on page 18, line 30, has been replaced with the following amended paragraph:

--Polynucleotide and polypeptide sequences may be aligned, and percentage of identical residues in a specified region may be determined against another polynucleotide or polypeptide sequence, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTX and BLASTP programs are available on the NCBI anonymous FTP server [(ftp://ncbi.nlm.nih.gov)] under /blast/executables, and from the National Center for Biotechnology Information (NCBI) National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894, USA. The BLASTN algorithm Version 2.0.4 [Feb-24-1998] and Version 2.0.6 [Sept-16-1998], set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP, and BLASTX, is described at NCBI's Internet website [at the URL http://www.ncbi.nlm.nih.gov/BLAST/newblast.html] and in the publication of Altschul et al., *Nucleic Acids Res.* 25:3389-3402, 1997.--

The paragraph beginning on page 19, line 19, has been replaced with the following amended paragraph:

--The computer algorithm FASTA is available on the Internet [at the ftp site ftp://ftp.virginia.edu/pub/fasta/], and from the University of Virginia by contacting David Hudson, Assistance Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA. Version 2.0u4 [February 1996], set to the default parameters described in the documentation and distributed with the algorithm, may be used in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 183:63-98, 1990.--

The paragraph beginning on page 23, line 25, has been replaced with the following amended paragraph:

--In certain embodiments, the DNA constructs of the present invention include an open reading frame coding for at least a functional portion of a polypeptide of the present invention or a variant thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for regulating gene expression, *i.e.*, the portion of the molecule that is capable of binding to, or interacting with, the promoter of the gene to be expressed. The DNA-binding domain(s) for certain of the inventive polypeptides are identified below in Table 2. These DNA binding domains were identified using PROSITE 15.0 pattern or profile sequences as listed in the PROSITE database. PROSITE is available [at http://www.expasy.ch/sprot/prosite.html] on the Internet and its use is described in Hofman et al., *Nucleic Acids Res.* 27:215-219, 1999; and in Bairoch, *Nucleic Acids Res.* 20:Suppl.2013-2018, 1992.--

The paragraph beginning on page 32, line 22, has been replaced with the following amended paragraph:

--In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, and potential for formation of loops and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example[, at URL http://www.horizonpress.com/pcr/]. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach and Dyksler, *PCR primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995.--

On page 42, line 2, the present title has been replaced with the following new title:
--POLYNUCLEOTIDES FOR USE IN THE MODIFICATION OF GENE TRANSCRIPTION--

In the claims:

Claim 30 has been cancelled.

Claims 2 and 33 have been amended as follows:

2. (Twice Amended) An oligonucleotide probe or primer comprising at least [10] 20 contiguous residues complementary to [10] 20 contiguous residues of SEQ ID NO: 2076.

33. (Amended) An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences that are degeneratively equivalent to SEQ ID NO: 2076;

(b) sequences having at least 75% identity to SEQ ID NO: 2076;

(c) sequences having at least 90% identity to SEQ ID NO: 2076; and

(d) sequences having at least 95% identify to SEQ ID NO: [1076] 2076,

wherein the polynucleotide encodes a Myb transcription factor.

The following new claim has been added:

--35. An isolated polynucleotide that encodes SEQ ID NO: 2249.--